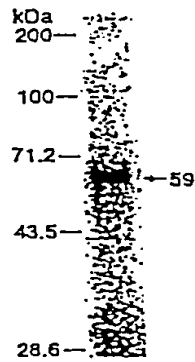


FIGURE 2



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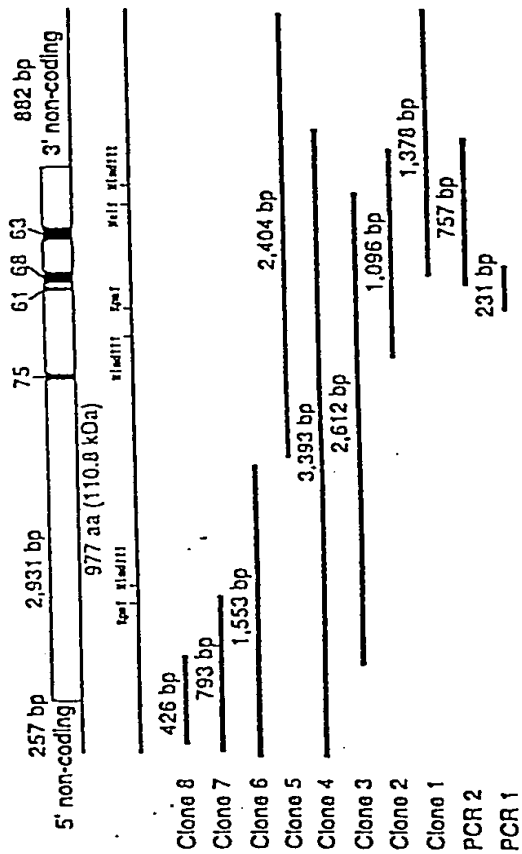
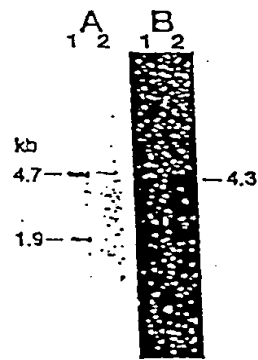


FIGURE 4

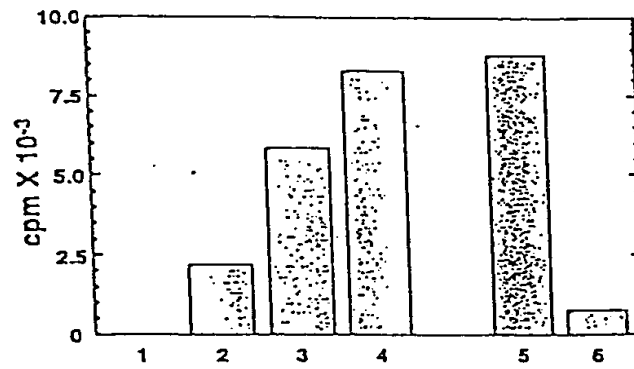


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FIGURE 5

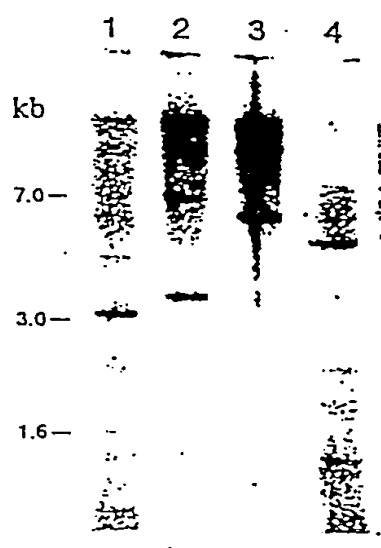
bPARG	(422)	ED...	KRKEQCEMKHQ RTE..RKIPKYI PPH	SEQ ID NO: 19
hPARG	(421)	ED...	RRKEQWETKHQ RTE..RKIPKYV PPH	SEQ ID NO: 20
mPARG	(413)	ED...	RRKEQCEVRHQ RTE..RKIPKYI PPN	SEQ ID NO: 21
CePARG	(29)	HQVPTMRRKLTEHGN	TESLLKEDPEEPKS	SEQ ID NO: 22
hPARG	(205)	EG...	KRKGD.EVDG.VDEVAKKSKKEKDK	SEQ ID NO: 23
mPARG	(205)	EG...	KRKGD.EVDG.TDEVAKKSKRKE TDK	SEQ ID NO: 24
bPARG	(208)	EG...	KRKGD.EVDG.IDEVTKKSKKEKDK	SEQ ID NO: 25
aPARG	(205)	EG...	KRKGE.EVDG..NVVAKKSKRKEKEK	SEQ ID NO: 26
XIPARG	(204)	EG...	KRKAD.EVDG.HSAATKKIKKEKEK	SEQ ID NO: 27
DmPARG	(202)	EELPDTKRAKM.ELS	DTNEEGEKKQR.....	SEQ ID NO: 28
SpPARG	(205)	EGVSSAKKAKI.EK	IDEEDAASIKELTEKIKK	SEQ ID NO: 29

FIGURE 6



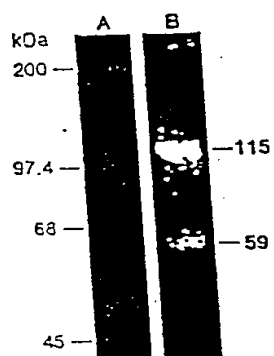
09973454 1005904
T0500T" T04E2060

FIGURE 7



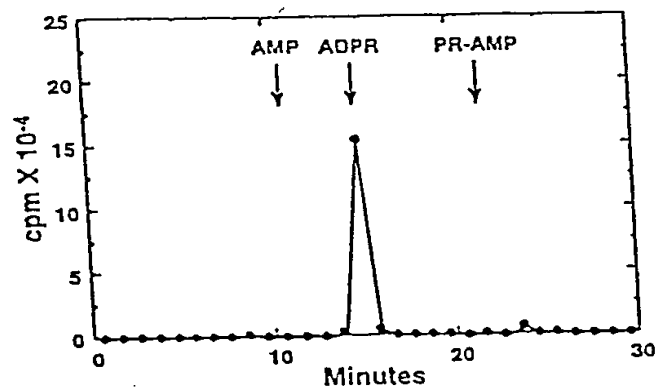
09973454.100904

FIGURE 8



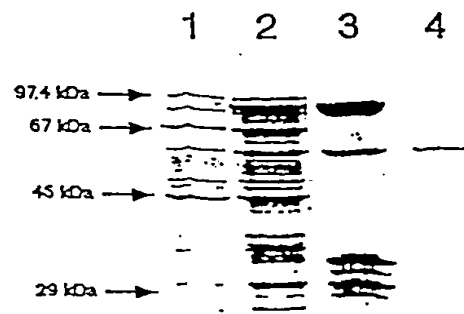
05973451-100501

FIGURE 9



09973454-100504
T05007-154660

FIGURE 10



09973454-100504
T0507 T04E2660

FIGURE 11

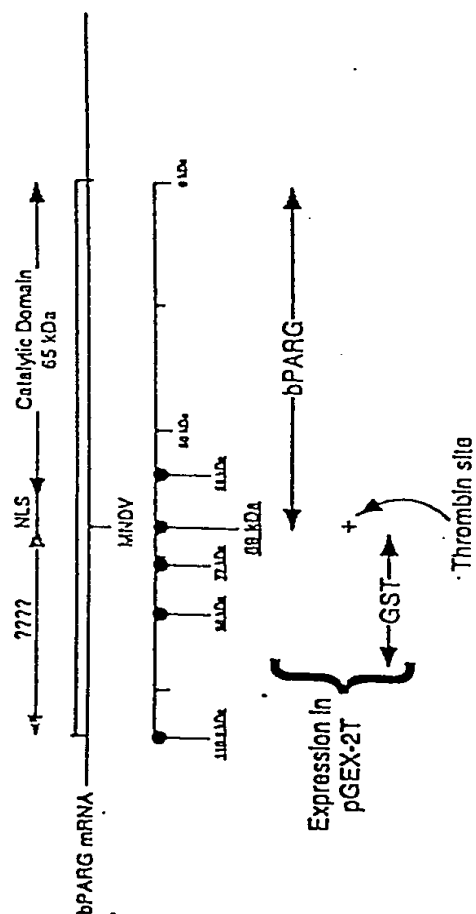
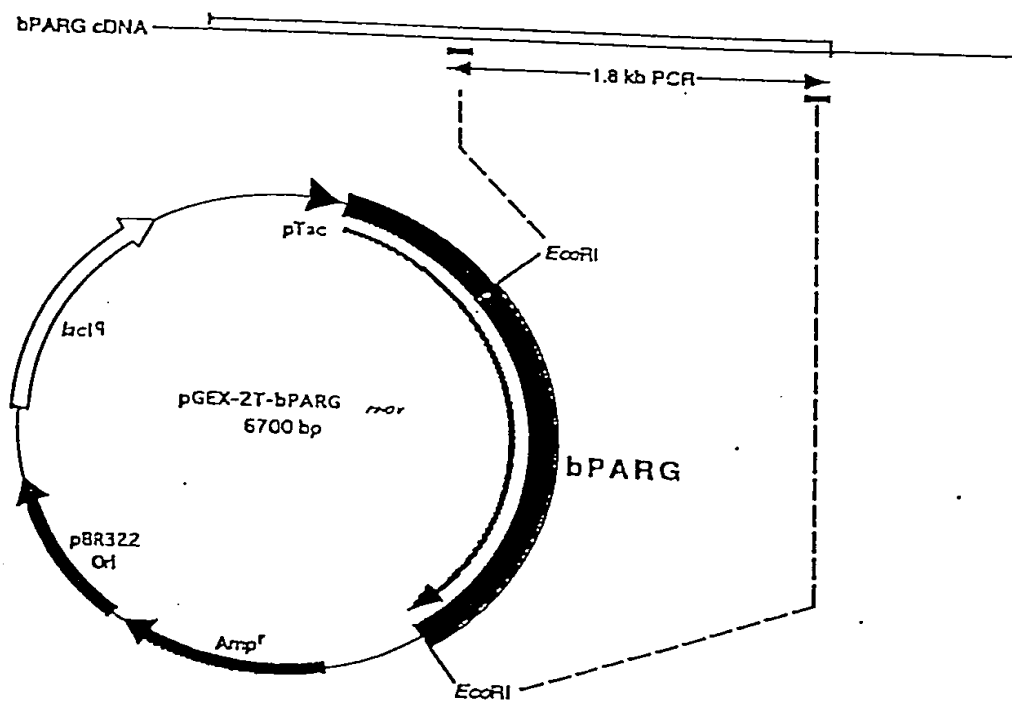


FIGURE 12



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FIGURE 13

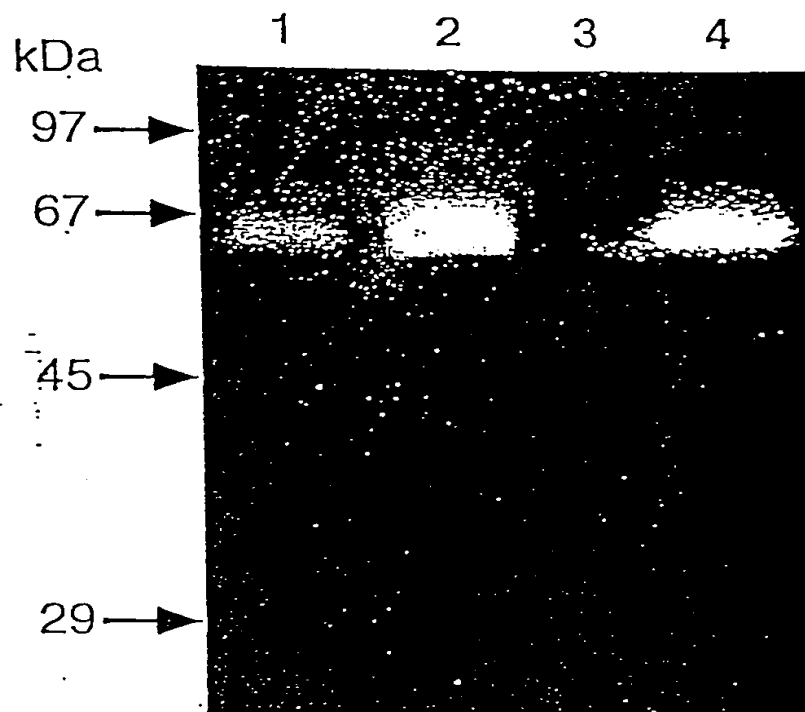
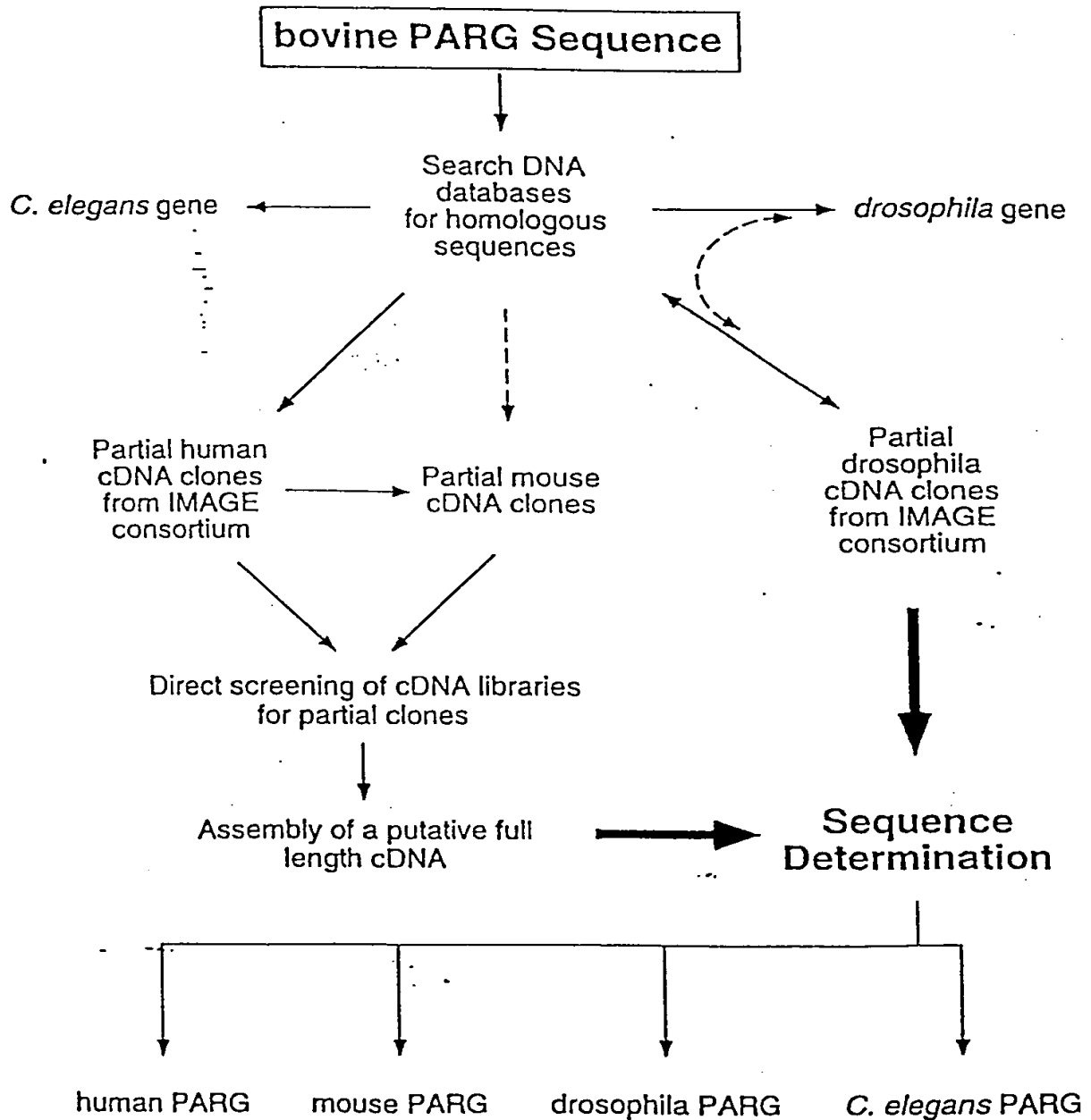


FIGURE 14

Strategy to Obtain Homologous PARG Sequences



Domain Organization of PARs

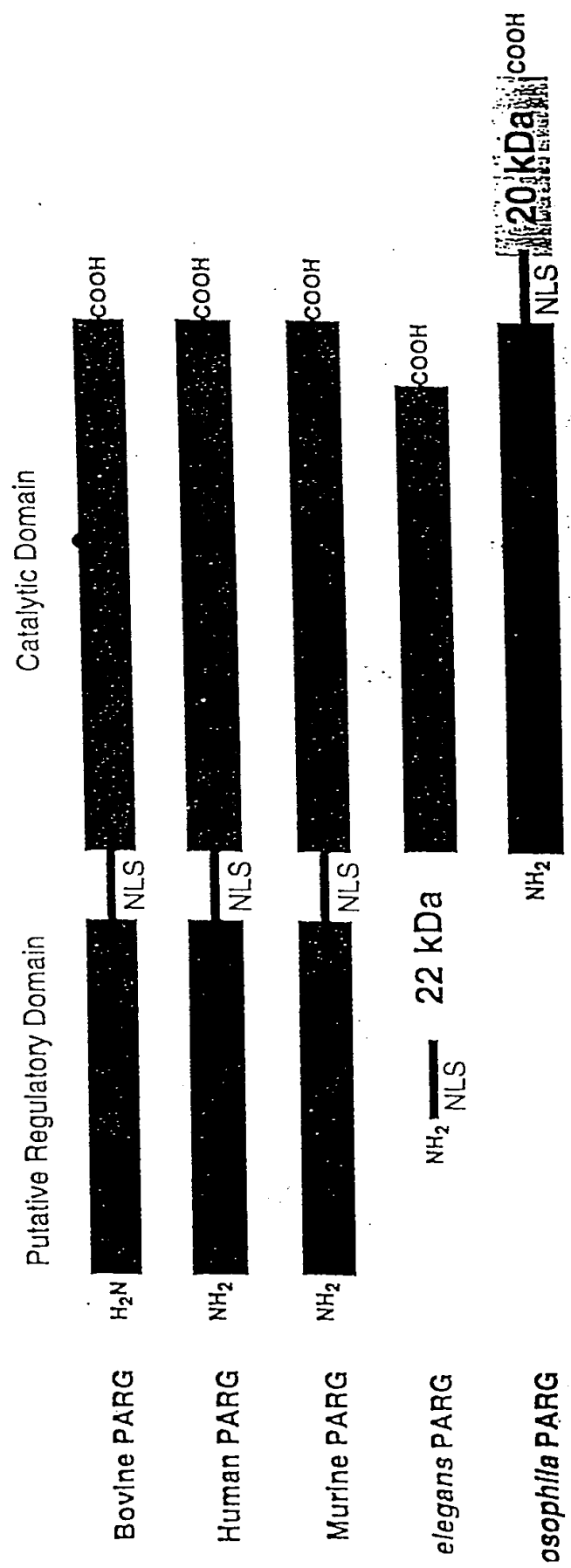


FIGURE 15

FIGURE 16

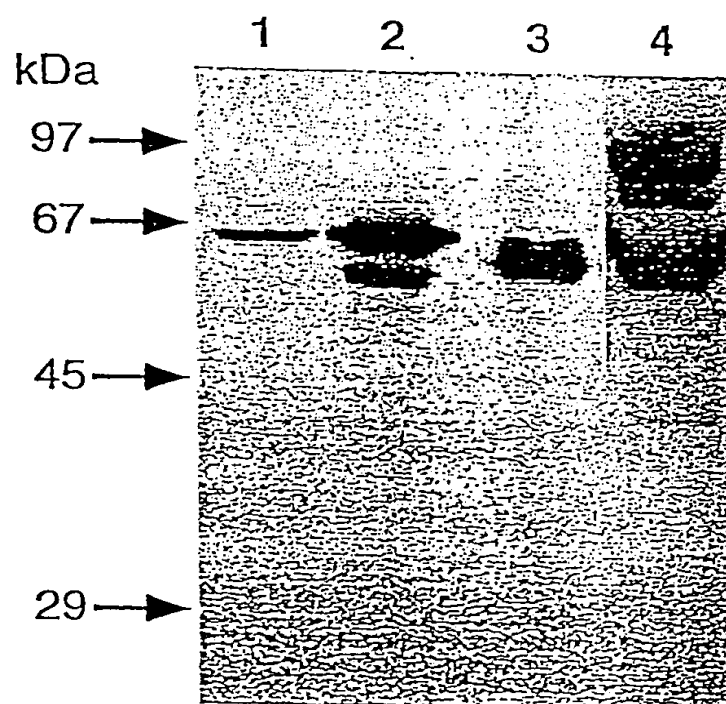
Multiple Alignment of Amino Acid Sequences of PARG from Different Species

```

parg 1 MSAGPGCEPCTKRPRNDAAATSPFAASDARSFPGRQRRVLDSKDAVPQVRVPPSSSQCALGRAGQHRGATSLSVFKQKTTISWMDTKGKIKTVESESLHSK
parg 1 MNAGPGCEPCTKRPRNDAAATSPFAASDARSFPGRQRRVLDSKDAHVQVRVPPSSPACVPGQAGQHRGATSLSVFKQKTTISWMDTKGKIKTAESESLDSK
parg 1 MSAGPGCEPCTKA.RNQAAGTSAPTASDSRSFPGRQRRVLDSKDAVPQVRVPPSSPACVSGRAGPFRGNATSFSVFKQKTTITWMDTKGPKTAESE...SK
parg 1 -----
parg 1 -----
parg 101 EENNTRRESMMSSSVQKDNFIQHNMKEKLENVSQLGFDKSPVEKGTQYLKQHQTAAMCKWQNEGPHSERLLESEPPAVTLVPEQFSNAKVDQSSPKDDHSDT
parg 100 EENNTRIESMMSSSVQKDNFIQHNVKELVHVSQSLDASLTKSTQILNQHQTAAMCKWQNEGPHTEQLLESEPPQTVTLVPEQFSNAKIDRSPQNDHSDT
parg 97 EENNTRIDSMMSSSVQKDNFIQHPKVEKLENVQNLNLDKSPTEKSSQYLNQHQTAASVCKWQNEGPHKAEQLLASEPPACTPLPKQLSNANIGQSPFTDDHSDT
parg 1 -----
parg 1 -----MSKKFIELGDPVTQDEKDIEDI
parg 201 NSRESRDNQQLTHVKL...ANAKQTMEDEQGREARSHQKCGKACHPAEACAGCQQEETDVSSESPLSDTGSEDVGTGLKNANRLNRQESSLGNSPFFFK
parg 200 DSENRDNDNQQLTTVKL...ANAKQTTEDEHAREAKSHQKCSKSCHPGEDCASCQDEIDVVPKSPLSVDSGEDVGTGSKNDKXLRQESCLGNHSPFFFK
parg 197 DSENRDNDNQQLTPIKL...ANTKPTVGDDQ...ARSHCKCSGSRQSVKDCGTGCQQEEDVLPSPLSVDSGAEDIGTGPKNDKXLTGQESSLGDSPFFFK
parg 1 -----
parg 23 VGVGFAHQVPTMKRRRLTEHGHTTESKEDPEEPKSRDVFVSSQSSDESQEDSAENPIAKEVSENCENLTETLKISNIESLDNVTERSEHTLDN...HK
parg 298 ESEPESPMDVDMSKNSCQDSEADEETSPGVDE.QEDSSSAQTANKPSRFPQREADTELKRSSAKGGEIRLHPQFEGQESRAGWN.DVNAKRPFGSTSSLN
parg 297 ESEPESPMDVDMSKNSCQDSEADEETSPGVDE.QEDGSSSQTAHXPSPRFPQARDADIEFKRISTKRGGEVRLHPQFEGQESRTGWN.DLNAKLPONISSLN
parg 291 ESEPESPMDVDMSKNSCQDSEADEETSPGVDE.QDDRS.QTANHLSSCQAREADGDLKRKRYLTGSEVRLHPQFE.GENNAOTS.DLNAKPSCHSSSLN
parg 1 -----MQEPRSLIFPIFQ.KVYQS.TANRRR.ASASVL.
parg 119 STEPHEE.DVNNKSHIDVAINSDEDELVLLENKEMRDGEQVQLS...QDLFADDQELIEYPGIMKDDTTQLDITDSSDKSIACVKKLPIETYPV
parg 396 VECRNSKQHGKRDSDKITDHFMRVPKAEKRRKQCEMKHQRTERRKIPKIPPHLSPKDKKWLGTPIEM...RMPRCGIRLPLLRPSANHTVTIRVDLLRIG
parg 395 VECRNSKQHGKRDSDKITDHFMRVPKAEKRRKQCEMKHQRTERRKIPKIPPHLSPKDKKWLGTPIEM...RMPRCGIRLPLLRPSANHTVTIRVDLLRAG
parg 387 VECRNSKQHGKRDSDKITDHFMRISKSEDRRKQCEVRHQRTERRKIPKIPPHLPPEKRWLGTPIEM...RMPRCGIRLPLLRPSASHTVTIRVDLLRAG
parg 32 .....TNRLOK...ALCLNCARMSKSPDGGISEIE...TEEE.PENLANSL...DSDWRGVSMHAHNRQPFELNHPVPTAGNLHRVMIQLPIRET.
parg 216 EDSKATKTIVTSSSSS...LSTVSTCEAPAKGRARMIQKELEKHVIAFTEGHNT...LQPDNLKVDPPDRNRY.CTIPNFPASQG...KLRED.NRIG
parg 494 EVPK.FPPTHPKDLWDNKHVKMPCSEONLIPVEDENGE.RAAGSRWELIQTALLNRLTRPQNLKDAILKINVAISKKNWDTALIDFWDKVLHBAEAQHLY
parg 493 EVPK.FPPTHYKDLWDNKHVKMPCSEONLIPVEDENGE.RTAGSRWELIQTALLNKFTRPQNLKDAILKINVAISKKNWDTALIDFWDKVLHBAEAQHLY
parg 485 EVPK.FPPTHYKDLWDNKHVKMPCSEONLIPVEDENGE.RTAGSRWELIQTALLNKFTRPQNLKDAILKINVAISKKNWDTALIDFWDKVLHBAEAQHLY
parg 115 .PPR.FIKSPGK..WDSEHVRLPCAPESKIPRENPDGS.TTIDFRNEMIERALLQPIKCEELQAAIISYHTTIRDQNHFRALHQLLDELDSESTRVFF
parg 303 ...PKIVLPQRMR.EDSRGR...RDSYFYFKRKLDOYLKCYKTTGTFMFVGLH.....NMWE..FDPDITIK...LPAL.EMIYKMSLVGRREV
parg 592 QSILPDMVKIALCLPNICTQPIPLLKQKMNHSITMSQEQIASLLANAFFCTFPRRNA.KMKSEYSSYPDINFHRLFEGRSSRKPEKLTFLCYFRRV..T
parg 591 QSILPDMVKIALCLPNICTQPIPLLKQKMNHSITMSQEQIASLLANAFFCTFPRRNA.KMKSEYSSYPDINFHRLFEGRSSRKPEKLTFLCYFRRV..T
parg 583 QSILPDMVKIALCLPNICTQPIPLLKQKMNHSITMSQEQIASLLANAFFCTFPRRNA.KMKSEYSSYPDINFHRLFEGRSSRKPEKLTFLCYFRRV..T
parg 210 EDLLPRIIRLALRLPDLIQSPVLLKHKHNASLSLQQQISCLLANAFCTFPRRNTLKRKSEYSTFPDINFHRLYQSTGPAVLKELKCIHIFRRVCTP
parg 384 LEKPARVARIKTAEDILPERIYRLVGDE.SATLSHKQCAALVARMFFA.....RDPSPFS.....FCRILSSDKSIACVKKLPIETYP.....
parg 689 EKK...PTGLVTFTRQS.L.ED.F.PEMERCEKLL..TRLVVTIEGTIEGNGQGMLOVDPANRFVGGGVTSAGLVQEEIRFLINPFLIVSRFLTTEVLDE
parg 688 EKK...PTGLVTFTRQS.L.ED.F.PEMERCEKPL..TRLVVTIEGTIEGNGQGMLOVDPANRFVGGGVTSAGLVQEEIRFLINPFLIVSRFLTTEVLDE
parg 680 EKK...PTGLVTFTRQS.L.ED.F.PEMERCEKPL..TRLVVTIEGTIEGNGQGMLOVDPANRFVGGGVTSAGLVQEEIRFLINPFLIVSRFLTTEVLDE
parg 310 ERDASNVTGTVTVFVRRSGLPEH.L.IDWSQSAAPLGDVPLHVDAGETIEDEGIGLLQVDPAKYLGGGVVLCGGCVQEEIRFVICPELLVGLKFLTTECLRP
parg 463 DKMSMDPDDGAVSF.RLTAKMDKDTFNEEM.KDKKLRLSLPEVEFFDEMLIEDTAL.CTQVDFANEHLGGGVVLCGGCVQEEIRFLMCPMMVGMHLLCEKMKQ
parg 779 NECLIIITGTEQISEITGIARTIRWA....RSHEDRSE.RDDMQRRTEIIVADALHFR.RYLD...QFVPEKIRRELHKAICGFLRPGVSEHNSAVA
parg 778 NECLIIITGTEQISEITGIARTIRWS....RSHEDGSE.RDDCERRCTEIVADALHFR.RYLD...QFVPEKMRRELHKAICGFLRPGVSEHNSAVA
parg 770 NECLIIITGTEQISEITGIARTIRNA....RSHEDGSE.RDDMQRRCTEIVADALHFR.RYLD...QFVPEKVRRELHKAICGFLRPGVSEHNSAVA
parg 408 FEALVMLQABRYISNITGYAGSFENS....GNFEDSTP.RDSSGRRQTAIVADALHFA.QSHH...QYREDIMERELHKAICGFVHVMVTPP..PGVA
parg 560 LEAISIVGAIYVSSITGTGHTLKNASLQPNESRQNTNEFRDRFGRRLRVETIAIDAILFKGSKLDCQTEQLNKANIIREMKKASIGFMSQGPXTNIP.IV
parg 868 TQWNGCGAFGGDARLKALIQILAAAAAERDVVYFTFGDSELMRDIIYSMTFLTERKLTVGK.VIKLLLRYYNEECRCNCSTPGP.....DIKLYPFIHA
parg 867 TQWNGCGAFGGDARLKALIQILAAAAAERDVVYFTFGDSELMRDIIYSMTFLTERKLTVGK.VIKLLLRYYNEECRCNCSTPGP.....DIKLYPFIHA
parg 859 TQWNGCGAFGGDARLKALIQILAAAAAERDVVYFTFGDSELMRDIIYSMTFLTERKLTVGK.VIKLLLRYYNEECRCNCSTPGP.....DIKLYPFIHA
parg 495 TQWNGCGAFGGDARLKALIQILAAAAAERDVVYFTFGDSELMRDIIYSMTFLTERKLTVGK.VIKLLLRYYNEECRCNCSTPGP.....DIKLYPFIHA
parg 659 TQWNGCGAFNGDKPLKFIQVIAAGVADRLPHFCSPGPELAACKKXIERMKQKDDVTLGKSCSPISF-----
parg 961 VESCTQTTNQPGQRTGA-----
parg 960 VESCAETADHSGQRTGT-----
parg 952 VESSAETDDMPGQKAGT-----
parg 590 KEELKKVRDVPPEGASARAGSSRVAGLGEKSETSAKSSPELNKQPARPQITITQSTDLLPAQLSQDNSNSSEDQALLMLSDDEANAMMEASLEAKS
parg 727 -----
parg 978 -----
parg 977 -----
parg 969 -----
parg 690 SVEISMSSTTSKTSSTATKSHGSGGRQLSLEMLDTHIEKGSASKRPRKSPNCSKAEGSASRSKEIDVTDKDEKDDIVD
parg 727 -----

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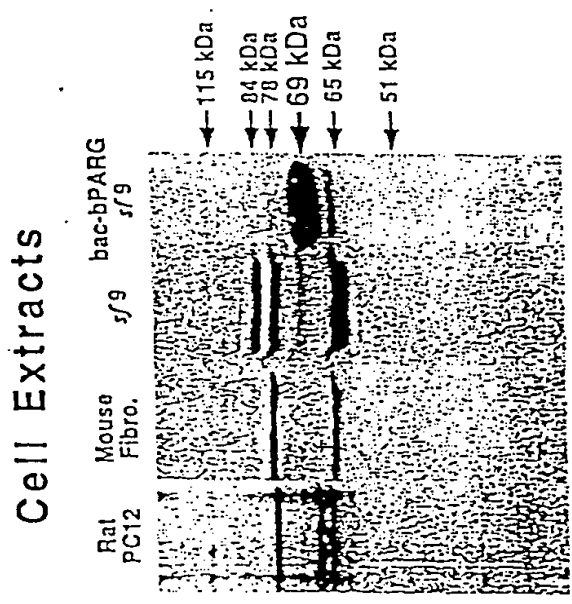

FIGURE 17



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FIGURE 18

B



A

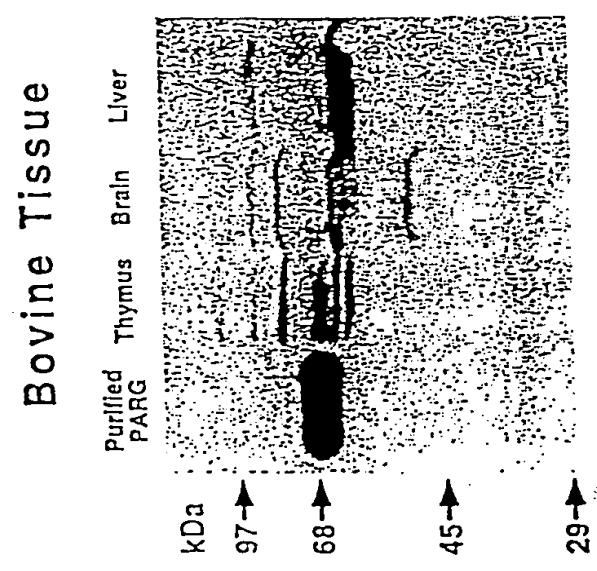
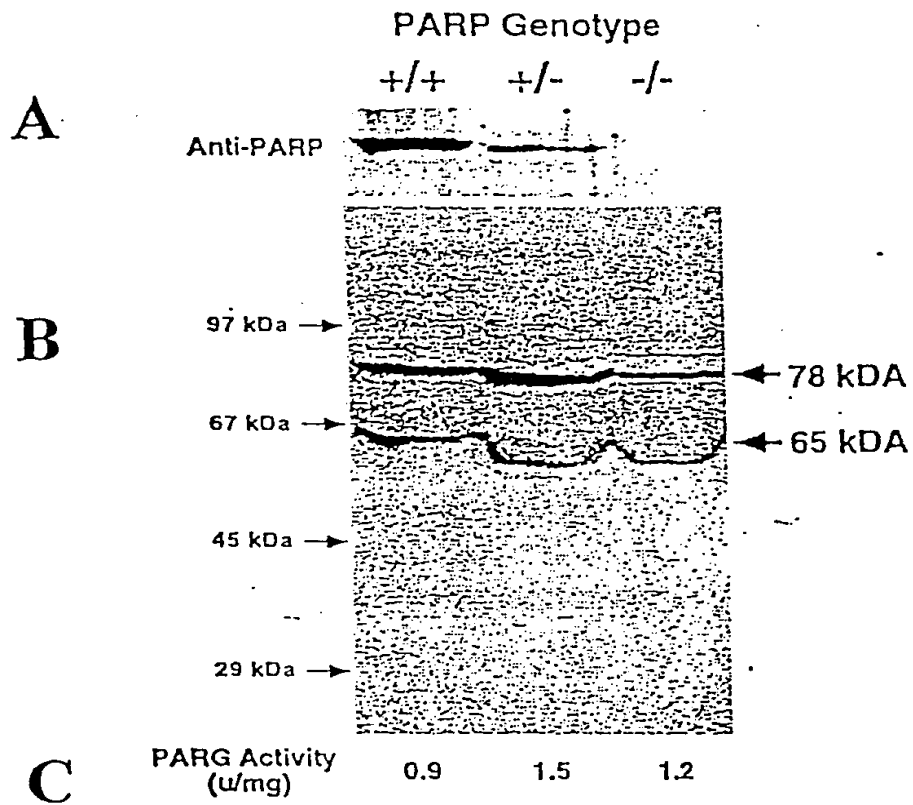


FIGURE 19



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Genomic cloning of the PARG gene

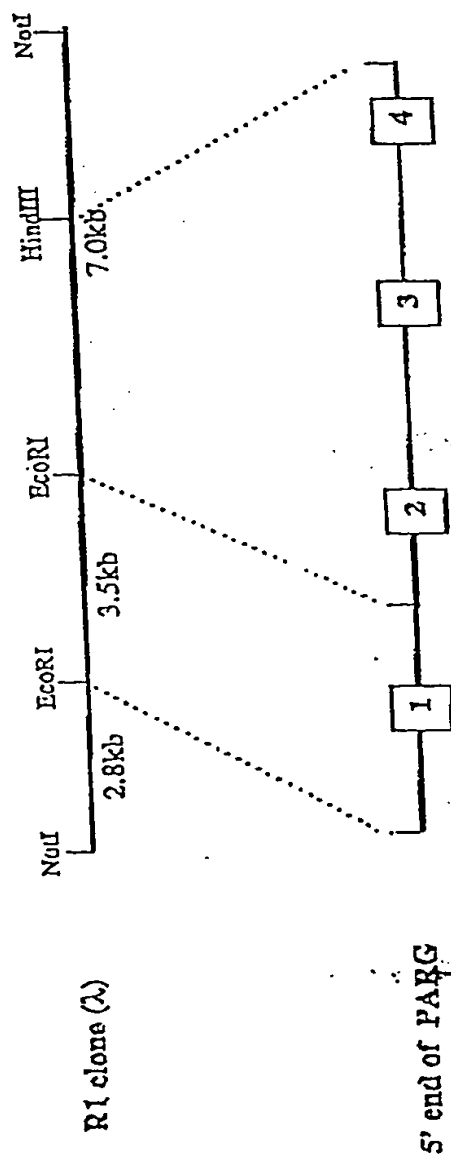


FIGURE 20

FIGURE 21
FOODOT" TSHZ660

